

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: TSUCHIYA, Masayuki
SATO, Koh
BENDIG, Mary Margaret
JONES, Steven Tarran
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(ii) TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
INTERLEUKIN-6 RECEPTOR

(iii) NUMBER OF SEQUENCES: 134

(iv) CORRESPONDENCE ADDRESS:
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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/114,285
(B) FILING DATE: 13-JUL-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/436,717
(B) FILING DATE: 08-MAY-1995

(viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/137,117
(B) FILING DATE: 20-DEC-1993

(ix) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: WO PCT/JP92/00544
(B) FILING DATE: 24-APR-1992

(x) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP 4-32084
(B) FILING DATE: 19-FEB-1992

(xi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP 3-95476
(B) FILING DATE: 25-APR-1991

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACTAGTCGAC ATGAAGTTGC CTGTTAGGCT GTTGGTGCTG

40

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACTAGTCGAC ATGGAGWCAG ACACACTCCT GYTATGGGT

39

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACTAGTCGAC ATGAGTGTGC TCACTCAGGT CCTGGSGTTG

40

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACTAGTCGAC ATGAGGRCCC CTGCTCAGWT TYTTGGMWTC TTG

43

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACTAGTCGAC ATGGATTTWC AGGTGCAGAT TWTCAGCTTC

40

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACTAGTCGAC ATGAGGCKCY YTGYTSAGYT YCTGRGG

37

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACTAGTCGAC ATGGGCWTCA AGATGGAGTC ACAKWYYCWG G

41

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACTAGTCGAC ATGTGGGGAY CTKTTTYCMM TTTTTCAATT G

41

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACTAGTCGAC ATGGTRTCBW CASCTCAGTT CCTTG

35

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACTAGTCGAC ATGTATATAT GTTTGTTGTC TATTTCCT

37

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACTAGTCGAC ATGGAAGCCC CAGCTCAGCT TCTCTTCC

38

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGATCCCGGG TGGATGGTGG GAAGATG

27

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACTAGTCGAC ATGAAATGCA GCTGGGTCA STTCTTC

37

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACTAGTCGAC ATGGGATGGA GCTRTATCAT SYTCTT

36

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACTAGTCGAC ATGAAGWTGT GGTTAACTG GGTTTTT

37

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACTAGTCGAC ATGRACCTTG GGYTCAGCTT GRTTT

35

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACTAGTCGAC ATGGACTCCA GGCTCAATT AGTTTCCTT

40

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACTAGTCGAC ATGGCTGTCY TRGSGCTRCT CTTCTGC

37

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACTAGTCGAC ATGGRATGGA GCKGGRTCTT TMTCTT

36

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ACTAGTCGAC ATGAGAGTGC TGATTCTTT GTG

33

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACTAGTCGAC ATGGMTTGGG TGTGGAMCTT GCTATTCCCTG

40

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACTAGTCGAC ATGGGCAGAC TTACATTCTC ATTCCCTG

37

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATCCCGGG CCAGTGGATA GACAGATG

28

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..393

(ix) FEATURE:

- (A) NAME/KEY: sig peptide
- (B) LOCATION: 1..60

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 61..393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATG GAG TCA GAC ACA CTC CTG CTA TGG GTA CTG CTG CTC TGG GTT CCA
Met Glu Ser Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
-20 -15 -10 -5

48

GGT TCC ACT GGT GAC ATT GTG CTG ACA CAG TCT CCT GCT TCC TTA GGT Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Gly 1 5 10	96
GTA TCT CTG GGG CAG AGG GCC ACC ATC TCA TGC AGG GCC AGC AAA AGT Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser 15 20 25	144
GTC AGT ACA TCT GGC TAT AGT TAT ATG CAC TGG TAC CAA CAG AAA CCA Val Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro 30 35 40	192
GGA CAG ACA CCC AAA CTC CTC ATC TAT CTT GCA TCC AAC CTA GAA TCT Gly Gln Thr Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser 45 50 55 60	240
GGG GTC CCT GCC AGG TTC AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr 65 70 75	288
CTC AAC ATC CAT CCT GTG GAG GAG GAT GCT GCA ACC TAT TAC TGT Leu Asn Ile His Pro Val Glu Glu Asp Ala Ala Thr Tyr Tyr Cys 80 85 90	336
CAG CAC AGT AGG GAG AAT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG Gln His Ser Arg Glu Asn Pro Tyr Thr Phe Gly Gly Thr Lys Leu 95 100 105	384
GAA ATA AAA Glu Ile Lys 110	393

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Glu Ser Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro -20 -15 -10 -5
Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Gly 1 5 10
Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser 15 20 25
Val Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro 30 35 40
Gly Gln Thr Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser 45 50 55 60
Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr 65 70 75

Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
80 85 90

Gln His Ser Arg Glu Asn Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
95 100 105

Glu Ile Lys
110

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..405

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..57

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 58..405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATG GGA TGG AGC GGG ATC TTT CTC TTC CTT CTG TCA GGA ACT GCA GGT	48
Met Gly Trp Ser Gly Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly	
-19 -15 -10 -5	
GTC CAC TCT GAG ATC CAG CTG CAG CAG TCT GGA CCT GAG CTG ATG AAG	96
Val His Ser Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys	
1 5 10	
CCT GGG GCT TCA GTG AAG ATA TCC TGC AAG GCT TCT GGT TAC TCA TTC	144
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe	
15 20 25	
ACT AGC TAT TAC ATA CAC TGG GTG AAG CAG AGC CAT GGA AAG AGC CTT	192
Thr Ser Tyr Tyr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu	
30 35 40 45	
GAG TGG ATT GGA TAT ATT GAT CCT TTC AAT GGT GGT ACT AGC TAC AAC	240
Glu Trp Ile Gly Tyr Ile Asp Pro Phe Asn Gly Gly Thr Ser Tyr Asn	
50 55 60	
CAG AAA TTC AAG GGC AAG GCC ACA TTG ACT GTT GAC AAA TCT TCC AGC	288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser	
65 70 75	
ACA GCC TAC ATG CAT CTC AGC AGC CTG ACA TCT GAG GAC TCT GCA GTC	336
Thr Ala Tyr Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val	
80 85 90	

TAT TAC TGT GCA AGG GGG GGT AAC CGC TTT GCT TAC TGG GGC CAA GGG	384
Tyr Tyr Cys Ala Arg Gly Gly Asn Arg Phe Ala Tyr Trp Gly Gln Gly	
95 100 105	
ACT CTG GTC ACT GTC TCT GCA	405
Thr Leu Val Thr Val Ser Ala	
110 115	

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Gly Trp Ser Gly Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
-19 -15 -10 -5

Val His Ser Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys
1 5 10

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe
15 20 25

Thr Ser Tyr Tyr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu
30 35 40 45

Glu Trp Ile Gly Tyr Ile Asp Pro Phe Asn Gly Gly Thr Ser Tyr Asn
50 55 60

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
65 70 75

Thr Ala Tyr Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
80 85 90

Tyr Tyr Cys Ala Arg Gly Gly Asn Arg Phe Ala Tyr Trp Gly Gln Gly
95 100 105

Thr Leu Val Thr Val Ser Ala
110 115

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..381

(ix) FEATURE:
(A) NAME/KEY: sig_peptide

(B) LOCATION: 1..60

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 61..381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATG GTG TCC TCA GCT CAG TTC CTT GGT CTC CTG TTG CTC TGT TTT CAA	48
Met Val Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Cys Phe Gln	
-20 -15 -10 -5	
GGT ACC AGA TGT GAT ATC CAG ATG ACA CAG ACT ACA TCC TCC CTG TCT	96
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Ser Ser Leu Ser	
1 5 10	
GCC TCT CTG GGA GAC AGA GTC ACC ATC AGT TGC AGG GCA AGT CAG GAC	144
Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp	
15 20 25	
ATT AGC AGT TAT TTA AAC TGG TAT CAG CAG AAA CCA GAT GGA ACT ATT	192
Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Ile	
30 35 40	
AAA CTC CTG ATC TAC ACA TCA AGA TTA CAC TCA GGA GTC CCA TCA	240
Lys Leu Leu Ile Tyr Tyr Ser Arg Leu His Ser Gly Val Pro Ser	
45 50 55 60	
AGG TTC AGT GGC AGT GGG TCT GGA ACA GAT TAT TCT CTC ACC ATT AAC	288
Arg Phe Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn	
65 70 75	
AAC CTG GAG CAA GAA GAC ATT GCC ACT TAC TTT TGC CAA CAG GGT AAC	336
Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn	
80 85 90	
ACG CTT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAT	381
Thr Leu Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile Asn	
95 100 105	

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Val Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Cys Phe Gln	
-20 -15 -10 -5	
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Ser Ser Leu Ser	
1 5 10	
Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp	
15 20 25	
Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Ile	
30 35 40	

Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
45 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn
65 70 75

Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn
80 85 90

Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Asn
95 100 105

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 411 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..411

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..54

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 55..411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATG AGA GTG CTG ATT CTT TTG TGG CTG TTC ACA GCC TTT CCT GGT ATC Met Arg Val Leu Ile Leu Leu Trp Leu Phe Thr Ala Phe Pro Gly Ile -18 -15 -10 -5	48
CTG TCT GAT GTG CAG CTT CAG GAG TCG GGA CCT GTC CTG GTG AAG CCT Leu Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Val Leu Val Lys Pro 1 5 10	96
TCT CAG TCT CTG TCC CTC ACC TGC ACT GTC ACT GGC TAC TCA ATC ACC Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr 15 20 25 30	144
AGT GAT CAT GCC TGG AGC TGG ATC CGG CAG TTT CCA GGA AAC AAA CTG Ser Asp His Ala Trp Ser Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu 35 40 45	192
GAG TGG ATG GGC TAC ATA AGT TAC AGT GGT ATC ACT ACC TAC AAC CCA Glu Trp Met Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro 50 55 60	240
TCT CTC AAA AGT CGA ATC TCT ATC ACT CGA GAC ACA TCC AAG AAC CAG Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln 65 70 75	288

TTC	TTC	CTA	CAG	TTG	AAT	TCT	GTG	ACT	ACT	GGG	GAC	ACG	TCC	ACA	TAT	336
Phe	Phe	Leu	Gln	Leu	Asn	Ser	Val	Thr	Thr	Gly	Asp	Thr	Ser	Thr	Tyr	
80					85					90						
TAC	TGT	GCA	AGA	TCC	CTA	GCT	CGG	ACT	ACG	GCT	ATG	GAC	TAC	TGG	GGT	384
Tyr	Cys	Ala	Arg	Ser	Leu	Ala	Arg	Thr	Thr	Ala	Met	Asp	Tyr	Trp	Gly	
95					100				105					110		
CAA	GGA	ACC	TCA	GTC	ACC	GTC	TCC	TCA								411
Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser								
					115											

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Arg Val Leu Ile Leu Leu Trp Leu Phe Thr Ala Phe Pro Gly Ile
-18 -15 -10 -5

Leu Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Val Leu Val Lys Pro
1 5 10

Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr
15 20 25 30

Ser Asp His Ala Trp Ser Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu
35 40 45

Glu Trp Met Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro
50 55 60

Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln
65 70 75

Phe Phe Leu Gln Leu Asn Ser Val Thr Thr Gly Asp Thr Ser Thr Tyr
80 85 90

Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly
95 100 105 110

Gln Gly Thr Ser Val Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 1..393

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..60

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 61..393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATG GAG TCA GAC ACA CTC CTG CTA TGG GTG CTG CTG CTC TGG GTT CCA	48
Met Glu Ser Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro	
-20 -15 -10 -5	
GGT TCC ACA GGT GAC ATT GTG TTG ATC CAA TCT CCA GCT TCT TTG GCT	96
Gly Ser Thr Gly Asp Ile Val Leu Ile Gln Ser Pro Ala Ser Leu Ala	
1 5 10	
GTG TCT CTA GGG CAG AGG GCC ACC ATA TCC TGC AGA GCC AGT GAA AGT	144
Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser	
15 20 25	
GTT GAT AGT TAT GGC AAT AGT TTT ATG CAC TGG TAC CAG CAG AAA CCA	192
Val Asp Ser Tyr Gly Asn Ser Phe Met His Trp Tyr Gln Gln Lys Pro	
30 35 40	
GGA CAG CCA CCC AAA CTC CTC ATC TAT CGT GCA TCC AAC CTA GAA TCT	240
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser	
45 50 55 60	
GGG ATC CCT GCC AGG TTC AGT GGC AGT GGG TCT AGG ACA GAC TTC ACC	288
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr	
65 70 75	
CTC ACC ATT AAT CCT GTG GAG GCT GAT GAT GTT GCA ACC TAT TAC TGT	336
Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys	
80 85 90	
CAG CAA AGT AAT GAG GAT CCT CCC ACG TTC GGT GCT GGG ACC AAG CTG	384
Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu	
95 100 105	
GAG CTG AAA	393
Glu Leu Lys	
110	

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Glu Ser Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro	
-20 -15 -10 -5	

Gly Ser Thr Gly Asp Ile Val Leu Ile Gln Ser Pro Ala Ser Leu Ala
1 5 10

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser
15 20 25

Val Asp Ser Tyr Gly Asn Ser Phe Met His Trp Tyr Gln Gln Lys Pro
30 35 40

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser
45 50 55 60

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr
65 70 75

Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys
80 85 90

Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu
95 100 105

Glu Leu Lys
110

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 417 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..417
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 1..57
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 58..417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ATG GGA TGG AGC GGG GTC TTT ATC TTC CTC CTG TCA GTA ACT GCA GGT 48
Met Gly Trp Ser Gly Val Phe Ile Phe Leu Leu Ser Val Thr Ala Gly
-19 -15 -10 -5

GTC CAC TCC CAG GTT CAA TTG CAG CAG TCT GGA GCT GAG TTG ATG AAG 96
Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Met Lys
1 5 10

CCT GGG GCC TCA GTC AAG ATC TCC TGC AAG GCT ACT GGC TAC ACA TTC 144
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe
15 20 25

AGT AGT TAT TGG ATA GTG TGG ATA AAG CAG AGG CCT GGA CAT GGC CTT Ser Ser Tyr Trp Ile Val Trp Ile Lys Gln Arg Pro Gly His Gly Leu 30 35 40 45	192
GAG TGG ATT GGA GAG ATT TTA CCT GGA ACC GGT AGT ACT AAC TAC AAT Glu Trp Ile Gly Glu Ile Leu Pro Gly Thr Gly Ser Thr Asn Tyr Asn 50 55 60	240
GAG AAA TTC AAG GGC AAG GCC ACA TTC ACT GCA GAT ACA TCT TCC AAC Glu Lys Phe Lys Gly Lys Ala Thr Phe Thr Ala Asp Thr Ser Asn 65 70 75	288
ACA GCC TAC ATG CAA CTC AGC AGC CTG ACA TCT GAG GAC TCT GCC GTC Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val 80 85 90	336
TAT TAC TGT GCA AGT CTA GAC AGC TCG GGC TAC TAT GCT ATG GAC TAT Tyr Tyr Cys Ala Ser Leu Asp Ser Ser Gly Tyr Tyr Ala Met Asp Tyr 95 100 105	384
TGG GGT CAA GGA ACC TCA GTC ACC GTC TCC TCA Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser 110 115 120	417

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Gly Trp Ser Gly Val Phe Ile Phe Leu Leu Ser Val Thr Ala Gly -19 -15 -10 -5
Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Met Lys 1 5 10
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe 15 20 25
Ser Ser Tyr Trp Ile Val Trp Ile Lys Gln Arg Pro Gly His Gly Leu 30 35 40 45
Glu Trp Ile Gly Glu Ile Leu Pro Gly Thr Gly Ser Thr Asn Tyr Asn 50 55 60
Glu Lys Phe Lys Gly Lys Ala Thr Phe Thr Ala Asp Thr Ser Ser Asn 65 70 75
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val 80 85 90
Tyr Tyr Cys Ala Ser Leu Asp Ser Ser Gly Tyr Tyr Ala Met Asp Tyr 95 100 105
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser 110 115 120

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..381

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..60

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 61..381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATG GTG TCC ACA CCT CAG TTC CTT GGT CTC CTG TTG ATC TGT TTT CAA	48
Met Val Ser Thr Pro Gln Phe Leu Gly Leu Leu Ile Cys Phe Gln	
-20 -15 -10 -5	
GGT ACC AGA TGT GAT ATC CAG ATG ACA CAG ACT ACA TCC TCC CTG TCT	96
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Ser Ser Leu Ser	
1 5 10	
GCC TCT CTG GGA GAC AGA GTC ACC ATC AGT TGC AGG GCA AGT CAG GAC	144
Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp	
15 20 25	
ATT AGT AAT TAT TTA AAC TGG TAT CAA CAG AAA CCA GAT GGA ACT GTT	192
Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val	
30 35 40	
AAA CTC CTG ATC TAC TAT ACA TCA AGA TTA CAC TCA GGA GTC CCA TCA	240
Lys Leu Ile Tyr Tyr Ser Arg Leu His Ser Gly Val Pro Ser	
45 50 55 60	
AGG TTC AGT GGC AGT GGG TCT GGA ACA GAT TAT TCT CTC ACC ATT AGC	288
Arg Phe Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser	
65 70 75	
AAC CTG GAG CAA GAA GAT ATT GCC AGT TAC TTT TGC CAA CAG GGT TAT	336
Asn Leu Glu Gln Glu Asp Ile Ala Ser Tyr Phe Cys Gln Gln Gly Tyr	
80 85 90	
ACG CCT CCG TGG ACG TTC GGT GGA GGC ACC AAG TTG GAA ATC AAA	381
Thr Pro Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys	
95 100 105	

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Val Ser Thr Pro Gln Phe Leu Gly Leu Leu Leu Ile Cys Phe Gln
-20 -15 -10 -5

Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser
1 5 10

Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp
15 20 25

Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val
30 35 40

Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
45 50 55 60

Arg Phe Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser
65 70 75

Asn Leu Glu Gln Glu Asp Ile Ala Ser Tyr Phe Cys Gln Gln Gly Tyr
80 85 90

Thr Pro Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
95 100 105

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..402

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..51

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 52..402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATG GAG CTG GAT CTT TAT CTT ATT CTG TCA GTA ACT TCA GGT GTC TAC
Met Glu Leu Asp Leu Tyr Leu Ile Leu Ser Val Thr Ser Gly Val Tyr
-17 -15 -10 -5 48

TCA CAG GTT CAG CTC CAG CAG TCT GGG GCT GAG CTG GCA AGA CCT GGG
Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly
1 5 10 15 96

GCT TCA GTG AAG TTG TCC TGC AAG GCT TCT GGC TAC ACC TTT ACT AAC Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn 20 25 30	144
TAC TGG GTG CAG TGG GTA AAA CAG AGG CCT GGA CAG GGT CTG GAA TGG Tyr Trp Val Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp 35 40 45	192
ATT GGG TCT ATT TAT CCT GGA GAT GGT GAT ACT AGG AAC ACT CAG AAG Ile Gly Ser Ile Tyr Pro Gly Asp Gly Asp Thr Arg Asn Thr Gln Lys 50 55 60	240
TTC AAG GGC AAG GCC ACA TTG ACT GCA GAT AAA TCC TCC ATC ACA GCC Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ile Thr Ala 65 70 75	288
TAC ATG CAA CTC ACC AGC TTG GCA TCT GAG GAC TCT GCG GTC TAT TAC Tyr Met Gln Leu Thr Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr 80 85 90 95	336
TGT GCA AGA TCG ACT GGT AAC CAC TTT GAC TAC TGG GGC CAA GGC ACC Cys Ala Arg Ser Thr Gly Asn His Phe Asp Tyr Trp Gly Gln Gly Thr 100 105 110	384
ACT CTC ACA GTC TCC TCA Thr Leu Thr Val Ser Ser 115	402

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Glu Leu Asp Leu Tyr Leu Ile Leu Ser Val Thr Ser Gly Val Tyr -17 -15 -10 -5
Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly 1 5 10 15
Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn 20 25 30
Tyr Trp Val Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp 35 40 45
Ile Gly Ser Ile Tyr Pro Gly Asp Gly Asp Thr Arg Asn Thr Gln Lys 50 55 60
Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ile Thr Ala 65 70 75
Tyr Met Gln Leu Thr Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr 80 85 90 95
Cys Ala Arg Ser Thr Gly Asn His Phe Asp Tyr Trp Gly Gln Gly Thr 100 105 110

Thr Leu Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ACAAAGCTTC CACCATGGAG TCAGACACAC TCCTG

35

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGCTAAGCTT CCACCATGGG ATGGAGCGGG ATCTTT

36

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTGGATCCA CTCACGTTTT ATTTCCAGCT TGGTC

35

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTTGGATCCA CTCACCTGCA GAGACAGTTA CCAGAG

36

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CTTGGATCCA CTCACGATTT ATTTCCAGCT TGGTC

35

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAAAGCTTC CACCAGGTG TCCTCAGCTC AGTTCC

36

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGTTAGATCT ACTCACCTGA GGAGACAGTG ACTGAGGTT

39

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTCTAAAGCTT CCACCATGAG AGTGCTGATT CTTTG

36

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TACGCAAACC GCCTCTC

17

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAGTGCACCA TATGCGGT

18

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACCGTGCTCG GCTACACCTT CACCAGCGAT CATGCCTGGA GCTGGGTGAG ACAGC

55

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TGAGTGGATT GGATACATTA GTTATAGTGG AATCACAACC TATAATCCAT CTCTCAAATC

60

CAG

63

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TATTATTGTG CAAGATCCCT AGCTCGGACT ACGGCTATGG ACTACTGGGG TCAA

54

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GTGACAATGC TGAGAGACAC CAGCAAG

27

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GGTGTCCACT -CCGATGTCCA -ACTG

24

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GGTCTTGAGT GGATGGGATA CATTAGT

27

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GTGTCTGGCT ACTCAAATTAC CAGCATCAT

29

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TGTAGAGCCA GCCAGGACAT CAGCAGTTAC CTGAACTGGT ACCAGCAG

48

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ATCTACTACA CCTCCAGACT GCACTCTGGT GTGCCAAGCA GA

42

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACCTACTACT GCCAACAGGG TAACACGCTT CCATACACGT TCGGCCAAGG

50

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

AGCGGTACCG ACTACACCTT CACCATC

27

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 706 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 8..52

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 135..146

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 147..503

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: join(8..52, 135..146, 147..503)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AAGCTTC ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala	49
-19 -15 -10	
ACA GGTAAAGGGGC TCACAGTAGC AGGCTTGAGG TCTGGACATA TATATGGGTG Thr -5	102
ACAATGACAT CCACCTTGCC TTTCTCTCCA CA GGT GTC CAC TCC CAG GTC CAA Gly Val His Ser Gln Val Gln	155
-4 1	
CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA CCT AGC CAG ACC CTG AGC Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln Thr Leu Ser	203
5 10 15	
CTG ACC TGC ACC GTG TCT GGC TAC TCA ATT ACC AGC GAT CAT GCC TGG Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp His Ala Trp	251
20 25 30 35	
AGC TGG GTG AGA CAG CCA CCT GGA CGA GGT CTT GAG TGG ATT GGA TAC Ser Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly Tyr	299
40 45 50	
ATT AGT TAT AGT GGA ATC ACA ACC TAT AAT CCA TCT CTC AAA TCC AGA Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu Lys Ser Arg	347
55 60 65	
GTG ACA ATG CTG AGA GAC ACC AGC AAG AAC CAG TTC AGC CTG AGA CTC Val Thr Met Leu Arg Asp Thr Ser Lys Asn Gln Phe Ser Leu Arg Leu	395
70 75 80	

AGC AGC GTG ACA GCC GCC GAC ACC GCG GTT TAT TAT TGT GCA AGA TCC	443
Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser	
85 90 95	
CTA GCT CGG ACT ACG GCT ATG GAC TAC TGG GGT CAA GGC AGC CTC GTC	491
Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly Ser Leu Val	
100 105 110 115	
ACA GTC TCC TCA GGTGAGTCCT TACAACCTCT CTCTTCTATT CAGCTTAAAT	543
Thr Val Ser Ser	
AGATTTACT GCATTTGTTG GGGGGAAAT GTGTGTATCT GAATTCAGG TCATGAAGGA	603
CTAGGGACAC CTTGGGAGTC AGAAAGGGTC ATTGGGAGCC CGGGCTGATG CAGACAGACA	663
TCCTCAGCTC CCAGACTTCA TGGCCAGAGA TTTATAGGGA TCC	706

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
Val His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg	
1 5 10	
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile	
15 20 25	
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly	
30 35 40 45	
Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn	
50 55 60	
Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn	
65 70 75	
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val	
80 85 90	
Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp	
95 100 105	
Gly Gln Gly Ser Leu Val Thr Val Ser Ser	
110 115	

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 8..52

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 135..146

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 147..467

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: join(8..52, 135..146, 147..467)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

AAGCTTC ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala -19 -15 -10	49
ACA GGTAAAGGGGC TCACAGTAGC AGGCTTGAGG TCTGGACATA TATATGGGTG Thr -5	102
ACAATGACAT CCACCTTGCC TTTCTCTCCA CA GGT GTC CAC TCC GAC ATC CAG Gly Val His Ser Asp Ile Gln -4 1	155
ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC AGC GTG GGT GAC AGA GTG Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val 5 10 15	203
ACC ATC ACC TGT AGA GCC AGC CAG GAC ATC AGC AGT TAC CTG AAT TGG Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp 20 25 30 35	251
TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG CTG CTG ATC TAC TAC ACC Tyr Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr 40 45 50	299
TCC AGA CTG CAC TCT GGT GTG CCA AGC AGA TTC AGC GGT AGC GGT AGC Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser 55 60 65	347
GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG GAC ATC Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile 70 75 80	395
GCT ACC TAC TAC TGC CAA CAG GGT AAC ACG CTT CCA TAC ACG TTC GGC Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly 85 90 95	443
CAA GGG ACC AAG GTG GAA ATC AAA CGTGAGTAGA ATTTAAACTT TGCTTCCTCA Gln Gly Thr Lys Val Glu Ile Lys 100 105	497
GTTGGATCC	506

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
1 5 10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile
15 20 25

Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
30 35 40 45

Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr
80 85 90

Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 12..425

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 12..68

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 69..425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

AAGCTTCCAC C ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA	50
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr	
-19 -15 -10	
GCT ACA GGT GTC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT	98
Ala Thr Gly Val His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly	
-5 1 5 10	
CTT GTG AGA CCT AGC CAG ACC CTG AGC CTG ACC TGC ACC GTG TCT GGC	146
Leu Val Arg Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly	
15 20 25	
TAC TCA ATT ACC AGC GAT CAT GCC TGG AGC TGG GTT CGC CAG CCA CCT	194
Tyr Ser Ile Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro	
30 35 40	
GGA CGA GGT CTT GAG TGG ATT GGA TAC ATT AGT TAT AGT GGA ATC ACA	242
Gly Arg Gly Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr	
45 50 55	
ACC TAT AAT CCA TCT CTC AAA TCC AGA GTG ACA ATG CTG AGA GAC ACC	290
Thr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr	
60 65 70	
AGC AAG AAC CAG TTC AGC CTG AGA CTC AGC AGC GTG ACA GCC GCC GAC	338
Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp	
75 80 85 90	
ACC GCG GTT TAT TAT TGT GCA AGA TCC CTA GCT CGG ACT ACG GCT ATG	386
Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met	
95 100 105	
GAC TAC TGG GGT CAA GGC AGC CTC GTC ACA GTC TCC TCA GGTGAGTGGAA	435
Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser	
110 115	
TCC	438

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
Val His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg	
1 5 10	
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile	
15 20 25	
Thr Ser Asp His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly	
30 35 40 45	

Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn
50 55 60

Pro Ser Leu Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn
65 70 75

Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
80 85 90

Tyr Tyr Cys Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp
95 100 105

Gly Gln Gly Ser Leu Val Thr Val Ser Ser
110 115

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 12..389

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 12..68

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 69..389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

AAGCTTCCAC C ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA	50
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr	
-19 -15 -10	
GCT ACA GGT GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC	98
Ala Thr Gly Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser	
-5 1 5 10	
CTG AGC GCC AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AGA GCC AGC	146
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser	
15 20 25	
CAG GAC ATC AGC AGT TAC CTG AAT TGG TAC CAG CAG AAG CCA GGA AAG	194
Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys	
30 35 40	
GCT CCA AAG CTG CTG ATC TAC TAC ACC TCC AGA CTG CAC TCT GGT GTG	242
Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val	
45 50 55	
CCA AGC AGA TTC AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC	290
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr	
60 65 70	

ATC AGC AGC CTC CAG CCA GAG GAC ATC GCT ACC TAC TAC TGC CAA CAG	338
Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln	
75 80 85 90	
GGT AAC ACG CTT CCA TAC ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC	386
Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile	
95 100 105	
AAA CGTGAGTGGA TCC	402
Lys	

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
1 5 10	
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile	
15 20 25	
Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40 45	
Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg	
50 55 60	
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr	
80 85 90	
Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

TAAGGATCCA CTCACCTGAG GAGACTGTGA CGAGGC

36

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATCAAGCTTC CACCATGGGA TGGAGCTGTA TC

32

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AATGGATCCA CTCACGTTG ATTTCCACCT

30

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CATGCCTGGA GCTGGGTTCG CCAGCCACCT GGA

33

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

TCCAGGTGGC TGGCGAACCC AGCTCCAGGC ATG

33

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CAGCAGAACG CAGGAAAGGC TCCAAAGCTG

30

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAGCTTTGGA GCCTTCCTG GCTTCTGCTG

30

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ACCTGTAGAG CCAGCAAGAG TGTTAGTACA TCTGGCTATA GTTATATGCA CTGGTACCA	60
CAGAAG	66

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GCTGGCTCTA CAGGT	15
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(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

AAGCTGCTGA TCTACCTTCC ATCCACCCCTG GAATCTGGTG TGCCAAGC	48
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(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GTAGATCAGC AGCTT	15
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(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GCTACCTACT ACTGCCAGCA CAGTAGGGAG ACCCCATACA CGTTCGGC

48

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CTGGCAGTAG GTAGC

15

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 12..401
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 12..68
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 69..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AAGCTTCCAC C ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr
-19 -15 -10

50

GCT ACA GGT GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC Ala Thr Gly Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser -5 1 5 10	98
CTG AGC GCC AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AGA GCC AGC Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser 15 20 25	146
AAG AGT GTT AGT ACA TCT GGC TAT AGT TAT ATG CAC TGG TAC CAG CAG Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln 30 35 40	194
AAG CCA GGA AAG GCT CCA AAG CTG CTG ATC TAC CTT GCA TCC AAC CTG Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu 45 50 55	242
GAA TCT GGT GTG CCA AGC AGA TTC AGC GGT AGC GGT ACC GAC Glu Ser Gly Val Pro Ser Arg-Phe Ser Gly-Ser Gly Ser Gly Thr Asp 60 65 70	290
TTC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG GAC ATC GCT ACC TAC Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr 75 80 85 90	338
TAC TGC CAG CAC AGT AGG GAG AAC CCA TAC ACG TTC GGC CAA GGG ACC Tyr Cys Gln His Ser Arg Glu Asn Pro Tyr Thr Phe Gly Gln Gly Thr 95 100 105	386
AAG GTG GAA ATC AAA CGTGAGTGGAA TCC Lys Val Glu Ile Lys 110	414

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly -19 -15 -10 -5
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val 15 20 25
Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly 30 35 40 45
Lys Ala Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly 50 55 60
Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe 65 70 75
Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln 80 85 90

His Ser Arg Glu Asn Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu
95 100 105

Ile Lys
110

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GGTTATTCCAT TCACTAGTTA TTACATACAC TGGGTTAGAC AGGCC

45

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

AGTGAATGAA TAACCGCTAG CTTTACA

27

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GAGTGGGTGG GCTATATTGA TCCTTTCAAT GGTGGTACTA GCTATAATCA GAAGTTCAAG

60

GGCAGGGT

69

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ATAGCCCACC CACTC

15

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GGGGGTAACC GCTTGCTTA CTGGGGACAG GGTACC

36

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AGCAAAGCGG TTACCCCTC TGGCGCAGTA GTAGAC

36

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CAAGGTTACC ATGACCGTGG ACACCTCTAC

30

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CACGGTCATG GTAACCTTGC CCTTGAACTT

30

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GGGCTCGAAT GGATTGGCTA TATTGATCCT

30

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

AGGATCAATA TAGCCAATCC ATTGAGGCC

30

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GTAAAACGAG GCCAGT

16

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AACAGCTATG ACCATGA

17

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 433 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 16..420

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 16..72

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 73..420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

AAGCTTGCCG CCACC ATG GAC TGG ACC TGG CGC GTG TTT TGC CTG CTC GCC
Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala
-19 -15 -10

51

GTG GCT CCT GGG GCC CAC AGC CAG GTG CAA CTA GTG CAG TCC GGC GCC	99
Val Ala Pro Gly Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala	
-5 1 5	
GAA GTG AAG AAA CCC GGT GCT TCC GTG AAA GTC AGC TGT AAA GCT AGC	147
Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser	
10 15 20 25	
GGT TAT TCA TTC ACT AGT TAT TAC ATA CAC TGG GTT AGA CAG GCC CCA	195
Gly Tyr Ser Phe Thr Ser Tyr Tyr Ile His Trp Val Arg Gln Ala Pro	
30 35 40	
GGC CAA GGG CTC GAG TGG GTG GGC TAT ATT GAT CCT TTC AAT GGT GGT	243
Gly Gln Gly Leu Glu Trp Val Gly Tyr Ile Asp Pro Phe Asn Gly Gly	
45 50 55	
ACT AGC TAT AAT CAG AAG TTC AAG GGC AAG GTT ACC ATG ACC GTG GAC	291
Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Val Thr Met Thr Val Asp	
60 65 70	
ACC TCT ACA AAC ACC GCC TAC ATG GAA CTG TCC AGC CTG CGC TCC GAG	339
Thr Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu	
75 80 85	
GAC ACT GCA TGC TAC TAC TGC GCC AGA GGG GGT AAC CGC TTT GCT TAC	387
Asp Thr Ala Cys Tyr Tyr Cys Ala Arg Gly Gly Asn Arg Phe Ala Tyr	
90 95 100 105	
TGG GGA CAG GGT ACC CTT GTC ACC GTC AGT TCA GGTGAGTGGA TCC	433
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser	
110 115	

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly	
-19 -15 -10 -5	
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
1 5 10	
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe	
15 20 25	
Thr Ser Tyr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	
30 35 40 45	
Glu Trp Val Gly Tyr Ile Asp Pro Phe Asn Gly Gly Thr Ser Tyr Asn	
50 55 60	
Gln Lys Phe Lys Gly Lys Val Thr Met Thr Val Asp Thr Ser Thr Asn	
65 70 75	

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Cys
80 85 90

Tyr Tyr Cys Ala Arg Gly Gly Asn Arg Phe Ala Tyr Trp Gly Gln Gly
95 100 105

Thr Leu Val Thr Val Ser Ser
110 115

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 433 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 16..420

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 16..72

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 73..420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AAGCTTGCCG CCACC ATG GAC TGG ACC TGG CGC GTG TTT TGC CTG CTC GCC Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala -19 -15 -10	51
GTG GCT CCT GGG GCC CAC AGC CAG GTG CAA CTA GTG CAG TCC GGC GCC Val Ala Pro Gly Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala -5 1 5	99
GAA GTG AAG AAA CCC GGT GCT TCC GTG AAA GTC AGC TGT AAA GCT AGC Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser 10 15 20 25	147
GGT TAT TCA TTC ACT AGT TAT TAC ATA CAC TGG GTT AGA CAG GCC CCA Gly Tyr Ser Phe Thr Ser Tyr Tyr Ile His Trp Val Arg Gln Ala Pro 30 35 40	195
GGC CAA GGG CTC GAA TGG ATT GGC TAT ATT GAT CCT TTC AAT GGT GGT Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asp Pro Phe Asn Gly Gly 45 50 55	243
ACT AGC TAT AAT CAG AAG TTC AAG GGC AAG GTT ACC ATG ACC GTG GAC Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Val Thr Met Thr Val Asp 60 65 70	291
ACC TCT ACA AAC ACC GCC TAC ATG GAA CTG TCC AGC CTG CGC TCC GAG Thr Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu 75 80 85	339

GAC ACT GCA GTC TAC TGC GCC AGA GGG GGT AAC CGC TTT GCT TAC	387
Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Gly Asn Arg Phe Ala Tyr	
90 95 100 105	
TGG GGA CAG GGT ACC CTT GTC ACC GTC AGT TCA GGTGAGTGGAA TCC	433
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser	
110 115	

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly	
-19 -15 -10 -5	
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
1 5 10	
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe	
15 20 25	
Thr Ser Tyr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	
30 35 40 45	
Glu Trp Ile Gly Tyr Ile Asp Pro Phe Asn Gly Gly Thr Ser Tyr Asn	
50 55 60	
Gln Lys Phe Lys Gly Lys Val Thr Met Thr Val Asp Thr Ser Thr Asn	
65 70 75	
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
80 85 90	
Tyr Tyr Cys Ala Arg Gly Gly Asn Arg Phe Ala Tyr Trp Gly Gln Gly	
95 100 105	
Thr Leu Val Thr Val Ser Ser	
110 115	

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GATAAGCTTG CCGCCACCAT GGACTGGACC TGGAGGGTCT TCTTCTTGCT GGCTGTAGCT	60
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CCAGGTGCTC ACTCCCAGGT GCAGCTTGTG 90

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CACTCCCAGG TGCAGCTTGT GCAGTCTGGA GCTGAGGTGA AGAAGCCTGG GGCCTCAGTG 60

AAGGTTTCCT GCAAGGCTTC TGGATACTCA 90

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TGCAAGGCTT CTGGATACTC ATTCACTAGT TATTACATAC ACTGGGTGCG CCAGGGCCCC 60

GGACAAAGGC TTGAGTGGAT GGGATATATT 90

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CTTGAGTGGA TGGGATATAT TGACCCTTTC AATGGTGGTA CTAGCTATAA TCAGAAGTTC 60

AAGGGCAGAG TCACCATTAC CGTAGACACA 90

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GTCACCATTA CCGTAGACAC ATCCGCGAGC ACAGCCTACA TGGAGCTGAG CAGCCTGAGA	60
TCTGAAGACA CGGCTGTGTA TTACTGTGCG	90

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

ACGGCTGTGT ATTACTGTGC GAGAGGGGGT AACCGCTTTG CTTACTGGGG CCAGGGAAACC	60
CTGGTCACCG TCTCCTCAGG TGAGTGGATC CGAC	94

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATAAGCTTG CCGCC	15
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(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GTCGGATCCA CTCAC

15

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 433 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 16..420

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 16..72

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 73..420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

AAGCTTGCCG CCACC ATG GAC TGG ACC TGG AGG GTC TTC TTG CTG GCT
Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala
-19 -15 -10

51

GTA GCT CCA GGT GCT CAC TCC CAG GTG CAG CTT GTG CAG TCT GGA GCT
Val Ala Pro Gly Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala
-5 1 5

99

GAG GTG AAG AAG CCT GGG GCC TCA GTG AAG GTT TCC TGC AAG GCT TCT
Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
10 15 20 25

147

GGA TAC TCA TTC ACT AGT TAT TAC ATA CAC TGG GTG CGC CAG GCC CCC
Gly Tyr Ser Phe Thr Ser Tyr Tyr Ile His Trp Val Arg Gln Ala Pro
30 35 40

195

GGA CAA AGG CTT GAG TGG ATG GGA TAT ATT GAC CCT TTC AAT GGT GGT
Gly Gln Arg Leu Glu Trp Met Gly Tyr Ile Asp Pro Phe Asn Gly Gly
45 50 55

243

ACT AGC TAT AAT CAG AAG TTC AAG GGC AGA GTC ACC ATT ACC GTA GAC
Thr Ser Tyr Asn Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Val Asp
60 65 70

291

ACA TCC GCG AGC ACA GCC TAC ATG GAG CTG AGC AGT CTG AGA TCT GAA	339
Thr Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu	
75 80 85	
GAC ACG GCT GTG TAT TAC TGT GCG AGA GGG GGT AAC CGC TTT GCT TAC	387
Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Gly Asn Arg Phe Ala Tyr	
90 95 100 105	
TGG GGC CAG GGA ACC CTG GTC ACC GTC TCC TCA GGTGAGTGG A TCC	433
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser	
110 115	

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly
-19 -15 -10 -5

Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
1 5 10

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
15 20 25

Thr Ser Tyr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu
30 35 40 45

Glu Trp Met Gly Tyr Ile Asp Pro Phe Asn Gly Gly Thr Ser Tyr Asn
50 55 60

Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Val Asp Thr Ser Ala Ser
65 70 75

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
80 85 90

Tyr Tyr Cys Ala Arg Gly Gly Asn Arg Phe Ala Tyr Trp Gly Gln Gly
95 100 105

Thr Leu Val Thr Val Ser Ser
110 115

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AGGCTTGAGT GGATTGGATA TATTGAC

27

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AAGTTCAAGG GCAAGGTCAC CATTACC

27

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GGTGCTTCGG TGAAAGTCAG CTGTAAAGCT

30

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AGCTTTACAG CTGACTTTCA CGGAAGCACC

30

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala
	20							25					30		
Pro	Lys	Leu	Leu	Ile	Tyr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly
	35						40					45			
Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp
	50					55						60			
Ile	Ala	Thr	Tyr	Tyr	Cys	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys
	65				70				75					80	

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Ser	Ser	Tyr
	20							25					30		
Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
				35				40				45			
Tyr	Tyr	Thr	Ser	Arg	Leu	His	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50						55				60				
Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro
	65				70				75					80	
Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Tyr
									90					95	
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys					
					100				105						

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Thr Phe Ser Trp Val
20 25 30

Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly Arg Val Thr Met
35 40 45

Leu Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Arg Leu Ser Ser Val
50 55 60

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Trp Gly Gln Gly
65 70 75 80

Ser Leu Val Thr Val Ser Ser
85

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Thr Phe Thr Ser Asp
20 25 30

His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp
35 40 45

Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Ser Leu Val Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Thr Phe Thr Ser Asp
20 25 30

His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp
35 40 45

Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Ser Leu Val Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Thr Phe Thr Ser Asp
20 25 30

His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp
35 40 45

Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Ser Leu Val Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Thr Phe Thr Ser Asp
20 25 30

His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp
35 40 45

Met Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Ser Leu Val Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Asp	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Arg	Pro	Ser	Gln
1					5					10					15
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Asp
					20			25						30	
His	Ala	Trp	Ser	Trp	Val	Arg	Gln	Pro	Pro	Gly	Arg	Gly	Leu	Glu	Trp
					35			40					45		
Met	Gly	Tyr	Ile	Ser	Tyr	Ser	Gly	Ile	Thr	Thr	Tyr	Asn	Pro	Ser	Leu
					50			55				60			
Lys	Ser	Arg	Val	Thr	Met	Leu	Arg	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser
					65			70			75			80	
Leu	Arg	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
					85				90				95		
Ala	Arg	Ser	Leu	Ala	Arg	Thr	Thr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly
					100				105				110		
Ser	Leu	Val	Thr	Val	Ser	Ser									
					115										

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Arg	Pro	Ser	Gln
1					5					10					15
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Tyr	Ser	Ile	Thr	Ser	Asp
					20			25						30	
His	Ala	Trp	Ser	Trp	Val	Arg	Gln	Pro	Pro	Gly	Arg	Gly	Leu	Glu	Trp
					35			40				45			
Ile	Gly	Tyr	Ile	Ser	Tyr	Ser	Gly	Ile	Thr	Thr	Tyr	Asn	Pro	Ser	Leu
					50			55				60			

Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Ser Leu Val Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Trp Tyr Gln Gln Lys Pro Gly Lys Ala
20 25 30

Pro Lys Leu Leu Ile Tyr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
35 40 45

Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp
50 55 60

Ile Ala Thr Tyr Tyr Cys Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

Gly	Tyr	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro
35							40				45				
Lys	Leu	Leu	Ile	Tyr	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Val	Pro	Ser	Arg
50						55				60					
Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser
65					70				75				80		
Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	His	Ser	Arg	Glu
	85							90				95			
Asn	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys		
	100							105				110			

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Glx	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Xaa
1				5					10				15		
Ser	Val	Xaa	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Ser	Trp	Val
	20							25				30			
Arg	Gln	Ala	Pro	Gly	Xaa	Gly	Leu	Glu	Trp	Val	Gly	Arg	Val	Thr	Xaa
	35						40				45				
Thr	Xaa	Asp	Xaa	Ser	Xaa	Asn	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu
	50					55				60					
Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Trp	Gly	Gln	Gly
	65					70			75		80				
Thr	Leu	Val	Thr	Val	Ser	Ser									
					85										

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10				15		

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Tyr Ile Asp Pro Phe Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Leu Asp Thr Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Arg Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Tyr Ile Asp Pro Phe Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Val Thr Met Thr Val Asp Thr Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Arg Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asp Pro Phe Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Leu Asp Thr Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Arg Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asp Pro Phe Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Val Thr Met Thr Val Asp Thr Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Arg Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: - - -
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Trp Val
20 25 30

Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Arg Val Thr Ile
35 40 45

Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu
50 55 60

Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Trp Gly Gln Gly
65 70 75 80

Thr Leu Val Thr Val Ser Ser
85

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: - - -
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asp Pro Phe Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Val Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Arg Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asp Pro Phe Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Val Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Arg Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asp Pro Phe Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Val Thr Ile Thr Val Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Arg Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asp Pro Phe Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Val Thr Ile Thr Val Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Asn Arg Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115